	Type	Hits	Search Text	DBs	Time Stamp
1	BRS	11515	(pin or multipin)near5(transfer$ or replicat$) or pinner	USPAT	2006/05/18 10:06
2	BRS	286	S7 same robot$	USPAT	2006/05/18 10:07
3	BRS	106	S7 same(analyte or blood or serum or microtiter or microtitre or multiwell)	USPAT	2006/05/18 10:08

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=> d his

     (FILE 'HOME' ENTERED AT 14:08:54 ON 18 MAY 2006)
     FILE 'CA' ENTERED AT 14:09:26 ON 18 MAY 2006
L1            45 S (LEHRACH H?/AU AND (NATURE/SO OR 1993/PY))OR(ROSENTHAL
A?/AU AND CRAXT!N M?/AU)
L2            29 S L1 NOT PY>1999
     FILE 'BIOSIS' ENTERED AT 14:11:23 ON 18 MAY 2006
L3            44 S L2
     FILE 'MEDLINE' ENTERED AT 14:11:34 ON 18 MAY 2006
L4            31 S L2
     FILE 'CA, BIOSIS, MEDLINE' ENTERED AT 14:11:53 ON 18 MAY 2006
L5            51 DUP REM L2 L3 L4 (53 DUPLICATES REMOVED)

=> d bib,ab l5 1-51

L5   ANSWER 23 OF 51  BIOSIS  STN
AN   1993:194280  BIOSIS
TI   An automated approach to generating expressed sequence catalogues.
AU   Meier-Ewert, Sebastian; Maier, Elmar; Ahmadi, Ali; Curtis, Jon; Lehrach,
     Hans
CS   Genome Analysis Lab., Imperial Cancer Res. Fund, 44 Lincoln's Inn
     Fields, PO Box 123, London WC2A 3PX, UK
SO   Nature (London), (1993) Vol. 361, No. 6410, pp. 375-376.

L5   ANSWER 29 OF 51  CA  COPYRIGHT 2006 ACS on STN
AN   118:140810  CA
TI   Large-scale production of DNA sequencing templates by microtitre format
     PCR
AU   Rosenthal, Andre; Coutelle, Oliver; Craxton, Molly
CS   Sch. Clin. Med., Univ. Cambridge, Cambridge, CB2 2QH, UK
SO   Nucleic Acids Research (1993), 21(1), 173-4
AB   A fast and reliable method is presented for sequencing plasmid and M13
     phage libraries based on PCR prodn. of sequencing templates in
     microtiter dishes, from cultures stored and grown in the same formate.
     This method consists of 4 steps: (1) Pick colonies or plaques into
     microtiter dishes and grow overnight; (2) Aliquot PCR mix with multi-
     channel pipet into PCR microtiter dish, load DNA using a 96-pin hedgehog
     device, and run PCR; (3) Remove excess primer, nucleotides and low-mol.-
     wt. truncated fragments by 1-step pptn. of templates with polyethylene
     glycol (PEG); (4) Cycle sequence PCR products using e.g. dye-terminator
     or dye primer chem. on the ABI 373A sequencer.  Lambda and M13 phage
     libraries may also be handled by a modification of steps 1 and 2.

=> log y
STN INTERNATIONAL LOGOFF AT 14:12:26 ON 18 MAY 2006

=> d his

     (FILE 'HOME' ENTERED AT 13:07:12 ON 18 MAY 2006)
     FILE 'CA' ENTERED AT 13:07:23 ON 18 MAY 2006
               E LEHRACH H/AU
L1          284 S E3-9 AND (CLONE OR CLONING)
L2            1 S L1 AND (PIN OR COMB)
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L3            20 S L1 AND ROBOT?
L4            76 S ROBOT? AND (PIN OR MULTIPIN OR COMB)
                 E ROSENTHAL A/AU
L5           161 S ROSENTHAL A?/AU AND DNA
L6            16 S L5 AND(AUTOMAT? OR ROBOT?)
L7           111 S L2-4,L6
     FILE 'BIOSIS' ENTERED AT 13:13:22 ON 18 MAY 2006
L8            36 S L7
     FILE 'MEDLINE' ENTERED AT 13:13:32 ON 18 MAY 2006
L9            47 S L7
     FILE 'CA, BIOSIS, MEDLINE' ENTERED AT 13:13:45 ON 18 MAY 2006
L10          137 DUP REM L7 L8 L9 (57 DUPLICATES REMOVED)

=> d bib,ab 1-137 l10
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L10 ANSWER 97 OF 137 CA COPYRIGHT 2006 ACS on STN
AN 131:140054 CA
TI Protein Microarrays for Gene Expression and Antibody Screening
AU Lueking, Angelika; Horn, Martin; Eickhoff, Holger; Bussow, Konrad; **Lehrach, Hans**; Walter, Gerald
CS Max Planck Institute for Molecular Genetics, Berlin, D-14195, Germany
SO Analytical Biochemistry (1999), 270(1), 103-111
AB Proteins translate genomic sequence information into function, enabling biol. processes. As a complementary approach to gene expression profiling on cDNA microarrays, we have developed a technique for high-throughput gene expression and antibody screening on chip-size protein microarrays. Using a picking/spotting **robot** equipped with a new transfer stamp, protein solns. were gridded onto polyvinylidene difluoride filters at high d. Specific purified protein was detected on the filters with high sensitivity (250 amol or 10 pg of a test protein). On a microarray made from bacterial lysates of 92 human cDNA **clones** expressed in a microtiter plate, putative protein expressors could be reliably identified. The rate of false-pos. **clones**, expressing proteins in incorrect reading frames, was low. Product specificity of selected **clones** was confirmed on identical microarrays using monoclonal antibodies. Cross-reactivities of some antibodies with unrelated proteins imply the use of protein microarrays for antibody specificity screening against whole libraries of proteins. Because this application would not be restricted to antigen-antibody systems, protein microarrays should provide a general resource for high-throughput screens of gene expression and receptor-ligand interactions.

L10 ANSWER 98 OF 137 CA COPYRIGHT 2006 ACS on STN
AN 131:28429 CA
TI Library picking, presentation and analysis
AU Bancroft, David R.; Maier, Elmar; **Lehrach, Hans**
CS GPC AG Genome Pharmaceuticals Corporation, Martinsreid, D-82152, Germany
SO Methods in Microbiology (1999), 28(Automation), 67-82
AB Arrayed genomic libraries and automated processes for screening and storing arrayed libraries are discussed. The authors use a gantry **robot** to integrate colony picking, gridding and rearraying functions in a single unit. The colony picking function uses a CCD camera and imaging software to identify colonies which are then transferred to wells in

microtiter plates. The gridding system transfers **clones** stored in microtiter plates to nylon membranes for high d. array hybridization. A large-scale thermocycling **robot** permits DNA amplification of library inserts to be performed directly in 384-well microtiter plates for applications such as genotyping or DNA sequencing which require purified insert DNA.

L10 ANSWER 102 OF 137 CA COPYRIGHT 2006 ACS on STN
AN 130:105812 CA
TI A method for global protein expression and antibody screening on high-density filters of an arrayed cDNA library
AU Bussow, Konrad; Cahill, Dolores; Nietfeld, Wilfried; Bancroft, David; Scherzinger, Eberhard; **Lehrach, Hans**; Walter, Gerald
CS Max Planck Institute for Molecular Genetics, Berlin, D-14195, Germany
SO Nucleic Acids Research (1998), 26(21), 5007-5008
AB We have developed a technique to establish catalogues of protein products of arrayed cDNA **clones** identified by DNA hybridization or sequencing. A human fetal brain cDNA library was directionally cloned in a bacterial vector that allows IPTG-inducible expression of His6-tagged fusion proteins. Using **robot** technol., the library was arrayed in microtiter plates and gridded onto high-d. in situ filters. A monoclonal antibody recognizing the N-terminal RGSH6 sequence of expressed proteins (RGS•His antibody, Qiagen) detected 20% of the library as putative expression **clones**. Two example genes, GAPDH and HSP90α, were identified on high-d. filters using DNA probes and antibodies against their proteins.

L10 ANSWER 107 OF 137 CA COPYRIGHT 2006 ACS on STN
AN 127:76640 CA
TI Simultaneous loading of 200 samples lanes for DNA sequencing on vertical and horizontal, standard and ultrathin gels
AU Erfle, H.; Ventzki, R.; Voss, H.; Rechmann, S.; Benes, V.; Stegemann, J.; Ansorge, W.
CS Biochemical Instrumentation, EMBL Heidelberg, Heidelberg, 69117, Germany
SO Nucleic Acids Research (1997), 25(11), 2229-2230
AB We have developed a simple and efficient technique for automated parallel loading of ≥200 lanes on a 30 cm-wide gel in automated DNA sequencing, using porous filter materials and an assocd. manual or **robotic** system. The samples are loaded onto the tree of a **comb** made of the porous material. The **comb**, with samples, is inserted directly above the straight edge of the polymd. gel. The samples are driven from the **comb** into the gel by the applied elec. field. A particularly advantageous aspect of this method is the elimination of the thin gel walls sepg. the sample wells in the std. gel loading technique. The time for sample loading is significantly reduced to a few minutes. The loading technique is applicable to horizontal or vertical systems, with std. or ultrathin gels.

L10 ANSWER 115 OF 137 CA COPYRIGHT 2006 ACS on STN
AN 121:100764 CA
TI Application of **robotic** technology to automated sequence fingerprint analysis by oligonucleotide hybridization
AU Maier, Elmar; Meier-Ewert, Sebastian; Ahmadi, Ali R.; Curtis, Jon;

Lehrach, Hans
CS Genome Analysis Laboratory and, London, WC2A 3PX, UK
SO Journal of Biotechnology (1994), 35(2-3), 191-203
AB The authors describe their prodn. line for the rapid anal. of large cDNA libraries applying **robotic** techniques to automatically pick, amplify, array, hybridize and analyze the **clones**. The authors also outline the current state of the hybridization techniques and describe anticipated future developments of the system. The authors' approach faces the large-scale anal. of cDNA **clones** with partial sequence anal. by oligonucleotide fingerprinting in the following way: after picking of individual colonies and arraying them automatically in quadruple d. (384-well) microtiter plates, the cDNA **clones** are amplified by an automated water-bath polymerase chain reaction (PCR), which allows the authors to run about 46 000 reactions in parallel. The PCR products are automatically transferred to nylon membranes in a high d. pattern using a **robotic** device. The authors routinely produce twelve 22 × 22 cm membranes in 90 min. Each membrane contains 20,736 **clones**, although much higher densities might be feasible using both miniaturized glass matrixes and fluorescence based hybridization techniques. Theor. anal. and preliminary computer simulations indicate that about 100-200 sequence specific hybridizations of octanucleotides to about 100,000 PCR products of 1000-1500 base-pairs length will generate sufficient information for classifying the **clones** into groups of identical or related genes and to identify a large no. of previously uncharacterized cDNA **clones**.

L10 ANSWER 118 OF 137 BIOSIS STN
AN 1993:164549 BIOSIS
TI Automated production of high density cosmid and YAC colony filters using a **robotic** workstation.
AU Olsen, A. S. [Reprint author]; Combs, J.; Garcia, E.; Elliott, J.; Amemiya, C.; De Jong, P.; Threadgill, G.
CS Biol. Biotechnology Res., L-452, Lawrence Livermore Natl. Lab., Livermore, CA 94550, USA
SO Biotechniques, (1993) Vol. 14, No. 1, pp. 116-117, 120-123.
AB We report here on a system for automated preparation of high-density colony filters of arrayed libraries using the high density replicating system (HDR) for the Beckman Biomek 1000 **robotic** workstation. This system, consisting of a 96-**pin** tool, a sterilization station and controlling software, transfers samples from microplates onto target membranes in arrays up to 36 times the density of a 96-well microplate. The transfer operation can be completely automated with the addition of the Biomek Side Loader System, which consists of a **robotic** arm capable of transferring plates and filters between the Biomek working tablet and a storage area. Using the complete system, we are able to plate 32 replica filters (8 times 12 cm), each containing the clones from 16 different microplates (i.e., 1536 clones per filter), in a 16-h overnight run without any operator intervention. We describe conditions used for transfer of bacterial yeast colonies and fixation of DNA to the membranes, and we illustrate hybridization results obtained with cosmid and YAC filters.

L10 ANSWER 120 OF 137 CA COPYRIGHT 2006 ACS on STN

AN 118:1597 CA
TI The development and application of automated gridding for efficient screening of yeast and bacterial ordered libraries
AU Bentley, D. R.; Todd, C.; Collins, J.; Holland, J.; Dunham, I.; Hassock, S.; Bankier, A.; Giannelli, F.
CS United Med. Dent. Sch., Guy's and St. Thomas's Hosp., London, SE1 9RT, UK
SO Genomics (1992), 12(3), 534-41
AB An automated gridding procedure for the inoculation of N yeast and bacterial clones in high-d. arrays has been developed. A 96-**pin** inoculating tool compatible with the std. microtiter plate format and an eight-position tablet have been designed to fit the Biomek 1000 programmable **robotic** workstation (Beckman Instruments). The system is used to inoculate 6 copies of 80 x 120-mm filters representing a total of ~20,000 individual clones in approx. 3 h. High-d. arrays of yeast artificial chromosome (YAC) and cosmid clones have been used for rapid large-scale hybridization screens of ordered libraries. In addn., an improved PCR library screening strategy has been developed using strips cut from the high-d. arrays to prep. row and column DNA pools for PCR anal. This strategy eliminates the final hybridization step and allows identification of a single clone by PCR in 2 days. The development of automated gridding technol. will have a significant impact on the establishment of fully versatile screening of ordered library resources for genomic studies.

L10 ANSWER 122 OF 137 CA COPYRIGHT 2006 ACS on STN
AN 116:77463 CA
TI The direct screening of cosmid libraries with YAC **clones**
AU Baxendale, S.; Bates, G. P.; MacDonald, M. E.; Gusella, J. F.; **Lehrach, H.**
CS Genome Anal. Lab., Imp. Cancer Res. Fund, London, WC2A 3PX, UK
SO Nucleic Acids Research (1991), 19(23), 6651
AB YAC **clones** can be difficult to analyze and manipulate and conversion of a YAC into cosmids provides a useful step in the characterization of the cloned region. Here a method is described for screening cosmid libraries directly with the human artificial chromosome. Two overlapping YAC **clones**, YGA5 (410 kb) and YGA10 (440 kb), that were isolated from a YAC library constructed from a 48XXXX human cell line, and which lie within the Huntington's disease gene candidate region on 4p16.3 were used. The yeast chromosomes were sepd. by pulsed field gel electrophoresis in LMP agarose (SeaPlaque GTG) and after staining with ethidium bromide, the human artificial chromosome was excised from the gel with the aid of UV irradn. (360 nm). After treatment with Geneclean (BIO 101), the DNA was resuspended in TE to 5 ng/μL. Approx. 50 ng of YAC DNA was labeled by random oligonucleotide priming with 40 μCi each of [α-32P]dGTP and [α-32P]dATP. Repetitive sequences were removed from probes by prehybridization with 1.5 mg/mL of sheared human placental DNA in 0.12 M Na2HPO4 pH 6.8 for 3 h at 65°. A flow sorted human chromosome 4 cosmid library, contained in 263 microtiter dishes, were spotted in high d. arrays onto Nylon membranes (Hybond N+) using a **robotic** device. Hybridizations were performed in 50% formamide at 42°. Filters were prehybridized with 100 μg/mL of denatured sonicated human placental DNA for 24 h and then hybridized with probes at a concn. of 106 cpm/mL. The

filters were washed and autoradiog. was for 2-3 days. The hybridization of YGA5 and YGA10 to a cosmid filter identified **clones** consistent with the expected coverage of the library and the size of each YAC insert. This technique allows immediate access to chromosome 4 DNA contained within chimeric YACs and **clones** contg. 2 artificial chromosomes.

L10 ANSWER 129 OF 137 CA COPYRIGHT 2006 ACS on STN
AN 112:49977 CA
TI A rapid semi-automated microtiter plate method for analysis and sequencing by PCR from bacterial stocks
AU Schofield, J. Paul; Vaudin, Mark; Kettle, Susan; Jones, D. Stephen C.
CS Mol. Genet. Unit, MRC, Cambridge, CB2 2QH, UK
SO Nucleic Acids Research (1989), 17(22), 9498
AB A semi-automated method is reported for screening and sequencing DNA libraries stored as frozen bacterial glycerol stocks in 96-well microtiter plates. A 96-prong replica plating **comb** is used to transfer bacterial cells from individual clones into sep. wells of a thermostable polycarbonate microtiter plate. A programmed **robotic** workstation is used to dispense a 10 μL polymerase chain reaction (PCR) mixt. into each well which is overlaid with mineral oil. The plates are incubated on a modified programmable thermocycler and target DNA is exposed by heating the soln. to 95° for 2 min prior to 30 cycles of amplification. This method allows the presence and size of inserts in 96 clones to be detd. within 4 h. This protocol was also used for direct sequencing of PCR products in which the amplification involved one biotinylated primer. This product was found to magnetic streptavidin beads and washed with NaOH and H2O. The single-stranded templates can be routinely sequenced manually using Sequenase or in a single well with fluorescently labeled dideoxynucleotides using an automated sequencer.

=> log y
STN INTERNATIONAL LOGOFF AT 13:14:53 ON 18 MAY 2006